Amendments In the Claims:

1-47. Cancelled.

B1

48. (New) A method for identifying a compound that potentially binds to a STAAU_R9 polypeptide, said method comprising:

- contacting a STAAU_R9 polypeptide comprising the amino acid sequence of SEQ ID NO: 2, or a biologically active fragment or a variant thereof, with a candidate compound in the presence of a bacteriophage polypeptide binding specifically to said STAAU_R9 polypeptide, biologically active fragment or variant;
- determining whether said candidate compound reduces said binding; and
- selecting a candidate compound reducing said binding.

49. (New) The method of claim 48, wherein said binding determination comprises detecting a protein:protein interaction between said STAAU_R9 polypeptide and said bacteriophage polypeptide.

50. (New) The method of claim 49, wherein detection of said protein:protein interaction comprises a measurement by a technique selected from the group consisting of phage display, surface plasmon resonance, fluorescence resonance energy transfer, fluorescence polarization changes, scintillation proximity assay affinity chromatography, biosensor assay, immuprecipitation, crosslinking, and yeast two hybrid.

51. (New) The method of claim 48, wherein said bacteriophage polypeptide is selected from the group consisting of phage 96ORF078 (SEQ ID NO: 4) and fragments or variants thereof.

52. (New) The method of claim 48, wherein said STAAU_R9 polypeptide comprises SEQ ID NO: 6.

53. (New) The method of claim 52, wherein said STAAU_R9 polypeptide is selected from the group consisting of residues 35-599, residues 229-599, residues 380-599, residues 449-599, residues 490-599, residues 530-599, and residues 561-599 from SEQ ID NO: 2.

54. (New) The method of claim 48, wherein said candidate compound is selected from the group consisting of small molecules, peptidomimetic compounds, peptides and polypeptides.

55. (New) A method for identifying a potential antibacterial agent, comprising:

contacting together: i) a bacteriophage polypeptide; ii) a bacterial primase polypeptide, and iii) at least one test compound, wherein said bacteriophage polypeptide and said primase polypeptide bind specifically to each other;

determining whether said test compound inhibits said binding; and

selecting any said test compound reducing said binding as a potential antibacterial agent.

56. (New) The method of claim 55, further comprising measuring the ability of the test compound selected in inhibiting either one or both of: (i) DNA binding activity of *S. aureus* DnaG primase and (ii) *S. aureus* DnaG primase-dependent DNA replication activity.

57. (New) The method of claim 55, further comprising measuring bactericidal or bacteriostatic activity of the test compound selected.

58. (New) The method of claim 55, wherein said test compound consists of a small molecule.

59. (New) A method for identifying a potential antibacterial agent, comprising:

contacting test compound with a functional biologically active fragment or variant of *S. aureus* DnaG primase having less than 566 amino acids;

determining whether said test compound inhibits or reduces the biological activity of said fragment; and

selecting any said test compound inhibiting or reducing said biological activity as a potential antibacterial agent.

60. (New) The method of claim 59, wherein said biological activity is selected from the group consisting of: *in vitro* or *in vivo* activation of DNA polymerase activity, RNA primase activity, stimulation of helicase activity of *S. aureus* DnaC helicase, stimulation of ATPase activity of *S. aureus* DnaC helicase, and binding a bacteriophage polypeptide.

61. (New) The method of claim 59, wherein said *S. aureus* DnaG primase fragment or variant comprises SEQ ID NO: 6.

62. (New) The method of claim 61, wherein said *S. aureus* DnaG primase fragment is selected from the group consisting of residues 35-599, residues 229-599, residues 380-599, residues 449-599, residues 490-599, residues 530-599, and residues 561-599 from SEQ ID NO: 2.

63. (New) The method of claim 59, further comprising measuring bactericidal or bacteriostatic activity of the test compound selected.

64. (New) The method of claim 59, wherein said candidate compound is selected from the group consisting of small molecules, peptidomimetic compounds, peptides and polypeptides.

65. (New) A method of making an antibacterial compound, comprising:

- identifying a candidate antibacterial compound by carrying out a method as defined in claim 12; and
- synthesizing or purifying said compound in an amount sufficient to provide a therapeutic effect when administered to an organism infected by *S. aureus*.

66. (New) An isolated, purified or enriched bacterial polypeptide fragment or variant that is derived from S. *aureus* DnaG primase comprising SEQ ID NO: 2, wherein said bacterial polypeptide fragment or variant binds a bacteriophage polypeptide.

67. (New) The bacterial polypeptide fragment or variant of claim 66, wherein said fragment or variant possess an biological activity selected from the group consisting of: *in vitro* or *in vivo*

activation of DNA polymerase activity, RNA primase activity, stimulation of helicase activity of *S. aureus* DnaC helicase and stimulation of ATPase activity of *S. aureus* DnaC helicase.

68. (New) The bacterial polypeptide fragment or variant of claim 66, wherein said bacteriophage polypeptide originates for bacteriophage 96.

69. (New) The bacterial polypeptide fragment or variant of claim 68, wherein said bacteriophage polypeptide is selected from the group consisting of 96ORF078 (SEQ ID NO: 4), and fragments or variants thereof.

70. (New) The bacterial polypeptide fragment or variant of claim 66, wherein said bacterial fragment or variant comprises a domain 100% identical to contiguous amino acids as set forth in SEQ ID NO: 2, said domain having less than 566 amino acids.

71. (New) The bacterial polypeptide fragment or variant of claim 70, wherein said fragment is selected from the group consisting of residues 35-599, residues 229-599, residues 380-599, residues 449-599, residues 490-599, residues 530-599, and residues 561-599 from SEQ ID NO: 2.

72. (New) A composition comprising a first polypeptide domain and a second polypeptide domain binding specifically with each other, wherein said first domain is derived from a STAAU_R9 polypeptide comprising SEQ ID NO: 2, and wherein said second domain is derived from a bacteriophage polypeptide binding to said STAAU_R9 polypeptide.

73. (New) A method for inhibiting a bacterium, comprising contacting the bacterium with a compound binding to a domain of *S. aureus* DnaG primase, said domain consisting essentially of residues 35 to 599 of SEQ ID NO: 2.

74. (New) The method of claim 73, wherein said domain comprises residues selected from the group consisting of residues 35-599, residues 229-599, residues 380-599, residues 449-599, residues 490-599, residues 530-599, and residues 561-599 from SEQ ID NO: 2.

75. (New) The method of claim 74, wherein said compound binds to a domain of said *S. aureus* DnaG primase consisting of SEQ ID NO: 6.

76. (New) The method of claim 73, wherein said compound consists of an antibacterial agent inhibiting the biological activity of said *S. aureus* DnaG primase.

77. (New) The method of claim 29, wherein said biological activity is selected from the group consisting of: *in vitro* or *in vivo* activation of DNA polymerase activity, RNA primase activity, stimulation of helicase activity of *S. aureus* DnaC helicase, stimulation of ATPase activity of *S. aureus* DnaC helicase, and binding a bacteriophage polypeptide.

78. (New) The method of claim 73, wherein said contacting is performed *in vivo* in a non-human animal.

79. (New) The method of claim 73, for treating or preventing a *S. aureus* infection.

80. (New) The method of claim 73, wherein said contacting is performed *in vitro*.

81. (New) A method for treating or preventing a bacterial infection in a mammal, comprising administering to said mammal a therapeutically effective or prophylactic effective amount of an antibacterial agent inhibiting the biological activity of a bacterial DnaG primase, wherein said antibacterial agent binds to a domain of a *S. aureus* DnaG primase, said domain consisting essentially of residues 561 to 599 of SEQ ID NO: 2.

82. (New) The method of claim 81, wherein said antibacterial agent inhibits the biological activity of said *S. aureus* DnaG primase.

83. (New) The method of claim 82, wherein said biological activity is selected from the group consisting of: *in vitro* or *in vivo* activation of DNA polymerase activity, RNA primase activity, stimulation of helicase activity of *S. aureus* DnaC helicase, stimulation of ATPase activity of *S. aureus* DnaC helicase, and binding a bacteriophage polypeptide.

Cont B1

84. (New) An isolated, purified or enriched polypeptide comprising at least 10 contiguous amino acid residues from amino acids 1 to 34 as set forth in SEQ ID NO: 2.

85. (New) An isolated, purified or enriched polypeptide comprising amino acids 1 to 34 as set forth in SEQ ID NO: 2.

86. (New) An isolated, purified or enriched polypeptide comprising an amino acid sequence having at least 95% identity over the entire length of SEQ ID NO: 2.

87. (New) An isolated, purified or enriched polypeptide comprising an amino acid sequence having at least 95% similarity over the entire length of SEQ ID NO: 2.

88. (New) An isolated, purified or enriched polypeptide consisting essentially of the amino acid sequence of SEQ ID NO: 2.

89. (New) An isolated, purified or enriched polypeptide comprising an amino acid sequence having at least 60% identity with amino acids 1 to 50 of SEQ ID NO: 2.

90. (New) An isolated, purified or enriched polypeptide comprising an amino acid sequence having at least 80% similarity with amino acids 1 to 50 of SEQ ID NO: 2.

91. (New) An isolated, purified or enriched biologically active primase, wherein said primase comprises a domain having an amino acid sequence selected from the group consisting of:

amino acid sequences comprising at least 10 contiguous amino acid residues from amino acids 1 to 34 as set forth in SEQ ID NO: 2;

amino acid sequences having at least 60% identity with amino acids 1 to 50 of SEQ ID NO: 2;

amino acid sequences having at least 80% similarity with amino acids 1 to 50 of SEQ ID NO: 2;

amino acid sequences having at least 95% identity over the entire length of SEQ ID NO: 2;

amino acid sequences having at least 95% similarity over the entire length of SEQ ID NO: 2; and

Cont B1

amino acid sequence set forth in SEQ ID NO: 2.

92. (New) An isolated polynucleotide consisting essentially of a nucleic acid molecule encoding a polypeptide as defined in claims 89 .

93. (New) An isolated polynucleotide encoding the biologically active primase of claim 91.

94. (New) A recombinant vector comprising a polynucleotide of claim 93.

95. (New) A recombinant cell comprising the vector of claim 94.

96. (New) An antibacterial agent having a bactericidal or bacteriostatic effect on *Staphylococcus aureus*, wherein said antibacterial agent inhibits bacterial DNA replication that is dependent on *S. aureus* DnaG primase activity.

97. (New) The antibacterial agent of claim 96, wherein said antibacterial agent binds specifically to a polypeptide which comprises the amino acid sequence of SEQ ID NO: 6.

98. (New) The antibacterial agent of claim 96, wherein said agent is selected from the group consisting of small organic molecules, peptidomimetic compounds, peptides, and polypeptides.

99. (New) The antibacterial agent of claim 98, wherein said polypeptide consists essentially of a bacteriophage protein.

100. (New) The antibacterial agent of claim 99, wherein said bacteriophage protein is selected from the group consisting of phage 96ORF078 (SEQ ID NO: 4) and fragments or variants thereof.

101. (New) The antibacterial agent of claim 96, wherein said agent reduces or decreases the biological activity of a *Staphylococcus aureus* polypeptide comprising SEQ ID NO: 6.

102. (New) An antibacterial composition comprising an antibacterial agent as defined in claim 96, and a pharmaceutically acceptable carrier.

103. (New) A method for inhibiting a bacterium, comprising contacting the bacterium with an antibacterial agent as defined in claim 96.

104. (New) The method of claim 103, wherein said contacting is performed *in vitro* or *in vivo*.